

SEQUENCE LISTING

<110> Bates, Elizabeth
Fournier, Nathalie
Chalus, Lionel
Garrone, Pierre

<120> MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS

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tggctcccc gtccttgga gaagaacaag gcc atg ggt cgg ccc ctg ctg ctg 174
Met Gly Arg Pro Leu Leu Leu
-19 -15

ccc cta ctg ccc ctg ctg ccg cca gca ttt ctg cag cct agt ggc 222
Pro Leu Leu Pro Leu Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly
-10 -5 1

tcc aca gga tct ggt cca agc tac ctt tat ggg gtc act caa cca aaa 270
Ser Thr Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys
5 10 15 20

cac ctc tca gcc tcc atg ggt ggc tct gtg gaa atc ccc ttc tcc ttc 318
His Leu Ser Ala Ser Met Gly Ser Val Glu Ile Pro Phe Ser Phe
25 30 35

tat tac ccc tgg gag tta gcc aca gct ccc gac gtg aga ata tcc tgg Tyr Tyr Pro Trp Glu Leu Ala Thr Ala Pro Asp Val Arg Ile Ser Trp 40 45 50	366
aga cgg ggc cac ttc cac ggg cag tcc ttc tac agc aca agg ccg cct Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro 55 60 65	414
tcc att cac aag gat tat gtg aac cgg ctc ttt ctg aac tgg aca gag Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu 70 75 80	462
ggc cag aag agc ggc ttc ctc agg atc tcc aac ctg cag aag cag gac Gly Gln Lys Ser Gly Phe Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp 85 90 95 100	510
cag tct gtg tat ttc tgc cga gtt gag ctg gac aca cgg agc tca ggg Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Ser Ser Gly 105 110 115	558
agg cag cag tgg cag tcc atc gag ggg acc aaa ctc tcc atc acc cag Arg Gln Gln Trp Gln Ser Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln 120 125 130	606
gct gtc acg acc acc acc cag agg ccc agc agc atg act acc acc tgg Ala Val Thr Thr Thr Gln Arg Pro Ser Ser Met Thr Thr Thr Trp 135 140 145	654
agg ctc agt agc aca acc acc aca acc ggc ctc agg gtc aca cag ggc Arg Leu Ser Ser Thr Thr Thr Thr Gly Leu Arg Val Thr Gln Gly 150 155 160	702
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aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat gag Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu 215 220 225	894
aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc aag Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys 230 235 240	942
gat gac ggc atc gta tat gct tcc ctt gcc ctc tcc agc tcc acc tca Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser 245 250 255 260	990

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Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu			
265	270		
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acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct caagactgaa	1092		
Thr Leu Tyr Ser Val Leu Lys Ala			
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tggtgaggcc aggtacagtg ggcacacacct gtaatcccag ctactctgaa gcctgaggca	1152		
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15	20	25	
Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala			
30	35	40	45
Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser			
50	55	60	
Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg			
65	70	75	
Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile			
80	85	90	
Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu			
95	100	105	
Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly			
110	115	120	125
Thr Lys Leu Ser Ile Thr Gln Ala Val Thr Thr Thr Thr Gln Arg Pro			
130	135	140	
Ser Ser Met Thr Thr Trp Arg Leu Ser Ser Thr Thr Thr Thr Thr			
145	150	155	
Gly Leu Arg Val Thr Gln Gly Lys Arg Arg Ser Asp Ser Trp His Ile			
160	165	170	

Ser Leu Glu Thr Ala Val Gly Val Ala Val Ala Val Thr Val Leu Gly
175 180 185

Ile Met Ile Leu Gly Leu Ile Cys Leu Leu Arg Trp Arg Arg Arg Lys
190 195 200 205

Gly Gln Gln Arg Thr Lys Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln
210 215 220

Asn Thr Glu Glu Pro Tyr Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr
225 230 235

Asp Pro Lys Leu Asn Pro Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu
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aacaaggcc atg ggt cgg ccc ctg ctg ccc cta ctg ccc ctg ctg
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-17 -15 -10 -5

ctg ccg cca gca ttt ctg cag cct agt ggc tcc aca gga tct ggt cca
Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro 216
1 5 10

agc tac ctt tat ggg gtc act caa cca aaa cac ctc tca gcc tcc atg
Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met 264
15 20 25

gg t ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta		312
Gly Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu		
30	35	40
gcc aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac		360
Ala Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His		
45	50	55
ggg cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat		408
Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr		
65	70	75
gtg aac cgg ctc ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc		456
Val Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe		
80	85	90
ctc agg atc tcc aac ctg cag aag cag gac cag tct gtg tat ttc tgc		504
Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys		
95	100	105
cga gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc		552
Arg Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser		
110	115	120
atc gag ggg acc aaa ctc tcc atc acc cag ggt cag cag cgg act aaa		600
Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys		
125	130	135
140		
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Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr		
145	150	155
gag aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc		696
Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro		
160	165	170
aag gat gac ggc atc gtc tat gct tcc ctt gcc ctc tcc agc tcc acc		744
Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr		
175	180	185
tca ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac		792
Ser Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn		
190	195	200
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Glu Thr Leu Tyr Ser Val Leu Lys Ala		
205	210	
caagactgaa tggtgaggcc aggtacagtg gcgcacacct gtaatcccag ctactctgaa		899
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 Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
 35 40 45

 Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
 50 55 60

 Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
 65 70 75

 Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
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 Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
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 Leu Asp Thr Arg Ser Ser Gly Arg Gin Gln Trp Gln Ser Ile Glu Gly
 115 120 125

 Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys Ala Thr Thr
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 Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu Asn Ile
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 Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys Asp Asp
 160 165 170 175

 Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser Pro Arg
 180 185 190

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cagacatctg tgcctcattc ctgatctcaa gggaaagca agaacaaggg aggcttcctc 180
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ggccctcagg cagccccctcc acagggccccc tctcctgcct ggacagctct gctggctcc 360
ccgtccccctg gagaagaaca aggcc atg ggt cgg ccc ctg ctg ctg ccc ctg 412
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Leu Leu Leu Leu Gln Pro Pro Ala Phe Leu Gln Pro Gly Gly Ser Thr
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Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu
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Ser Ala Ser Met Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr
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ccc tgg gag tta gcc ata gtt ccc aac gtg aga ata tcc tgg aga cgg 604
Pro Trp Glu Leu Ala Ile Val Pro Asn Val Arg Ile Ser Trp Arg Arg
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ggc cac ttc cac ggg cag tcc ttc tac agc aca agg ccg cct tcc att 652
Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile
60 65 70

cac aag gat tat gtg aac cgg ctc ttt ctg aac tgg aca gag ggt cag 700
His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln
75 80 85

gag agc ggc ttc ctc agg atc tca aac ctg cgg aag gag gac cag tct 748
Glu Ser Gly Phe Leu Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln Ser
90 95 100

gtg tat ttc tgc cga gtc gag ctg gac acc cgg aga tca ggg agg cag 796
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Leu Arg Val Thr Glu Ser Lys Gly His Ser Glu Ser Trp His Leu Ser			
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Leu Asp Thr Ala Ile Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr			
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ttaaaccact ggcatttggg ggctgttat tatagcagtg caaagagttc ctttatcctc		1386	
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Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly		
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Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala		
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Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly		
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Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val		
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aac cggtt ctc ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc ctc	459	
Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu		
80 85 90		
agg atc tcc aac ctg cag aag cag cag tct gtg tat ttc tgc cga	507	
Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg		
95 100 105		
gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc, atc	555	
Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile		
110 115 120 125		
gag ggg acc aaa ctc tcc atc acc cag ggg aac cct tcc aaa aca cag	603	
Glu Gly Thr Lys Leu Ser Ile Thr Gin Gly Asn Pro Ser Lys Thr Gln		
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Arg Ser His Met Arg Ile Ser Gly Met Lys Asp Lys Ile Gln Ile Pro		
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Ser		
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Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
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Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
50 55 60

Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
65 70 75

Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu
80 85 90

Arg Ile Ser Asn Leu Gln Lys Gln Asp Gin Ser Val Tyr Phe Cys Arg
95 100 105

Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gin Ser Ile
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 -15 -10 -5

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 Pro Pro Ala Phe Leu Gln Pro Gly Gly Ser Thr Gly Ser Gly Pro Ser
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 Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
 15 20 25

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 Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
 30 35 40 45

 aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac ggg 542
 Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
 50 55 60

 cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat gtg 590
 Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
 65 70 75

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 Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu
 80 85 90

 agg atc tca aac ctg cgg aag gag gac cag tct gtg tat ttc tgc cga 686
 Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg
 95 100 105

 gtc gag ctg gac acc cgg aga tca ggg agg cag cag ttg cag tcc atc 734
 Val Glu Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile
 110 115 120 125

 aag ggg acc aaa ctc acc atc acc cag gct gtc aca acc acc acc acc 782
 Lys Gly Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr
 130 135 140

 tgg agg ccc agc agc aca acc acc ata gcc ggc ctc agg gtc aca gaa 830
 Trp Arg Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu
 145 150 155

 agc aaa ggg cac tca gaa tca tgg cac cta agt ctg gac act gcc atc 878
 Ser Lys Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile
 160 165 170

agg gtt gca ttg gct gtc gct gtg ctc aaa act gtc att ttg gga ctg 926
 Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu
 175 180 185

ctg tgc ctc ctc ctg tgg tgg agg aga agg aaa ggt agc agg gcg cca 974
 Leu Cys Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro
 190 195 200 205

agc agt gac ttc tga ccaacagagt gtggggagaa gggatgtgta ttagccccgg 1029
 Ser Ser Asp Phe

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Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
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Val Glu Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile
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Lys Gly Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr
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